

ABSTRACT

Compositions and methods for the analysis of multiple nucleic acid target sequences are disclosed. The compositions comprise a probe comprising a target-specific portion for sequence-specific hybridization to a target nucleic acid sequence, and a tag; and a mobility-modifier comprising a tail and a tag complement for binding to the tag. The associated methods generally comprise the steps of providing a sample potentially containing one or more target nucleic acid sequences; providing one or more probes, each probe comprising a target-specific portion and a tag; providing one or more mobility modifiers, each mobility modifier comprising a tag complement and a tail; contacting the probe(s) and the target nucleic acid sequence(s) under conditions effective for sequence-dependent hybridization of the probe(s) and the target nucleic acid sequence(s); contacting the probe(s) and the mobility-modifier(s) under conditions suitable for selectively binding the probe(s) to the mobility modifier(s), thereby forming one or more a probe/mobility modifier complex(s); and analyzing the probe/mobility modifier complex(s) using a mobility-dependent analysis technique.

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